

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2011; month=3; day=9; hr=10; min=5; sec=19; ms=155;]

=====

Application No: 10569000 Version No: 4.0

Input Set:

Output Set:

Started: 2011-03-01 18:47:41.474
Finished: 2011-03-01 18:47:45.877
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 403 ms
Total Warnings: 1
Total Errors: 0
No. of SeqIDs Defined: 44
Actual SeqID Count: 44

| Error code | Error Description |
|------------|---|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (44) |

SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.
 Hannah, L. Curtis
 Iyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose
 Pyrophosphorylase

<130> UF.371XC1

<140> 10569000

<141> 2011-03-01

<150> PCT/US2004/026965

<151> 2004-08-18

<150> 60/496,188

<151> 2003-08-18

<160> 44

<170> PatentIn version 3.5

<210> 1

<211> 1425

<212> DNA

<213> zea mays

<400> 1

| | |
|---|-----|
| atggacatgg ctttggcgtc taaagcctcc cctccgccat ggaatgccac cgccgccgag | 60 |
| cagccaattc caaagcgtga caaagccgct gcaaatgatt caacatacct caatcctcaa | 120 |
| gctcatgata gtgttcttgg aatcattctg ggaggtggtg ctgggactag attgtacccc | 180 |
| ttgacaaaga agcgtgccaa gcctgcagtg ccattgggtg ccaactatag actgattgat | 240 |
| attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtgct aacgcaatth | 300 |
| aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtac | 360 |
| aagaatgaag ggtttgttga agtcttagct gcacagcaga gccagataa tccaaactgg | 420 |
| tttcagggtg ctgcagatgc tgtaaggcag tacttgtggt tgtttgagga gcataatgtg | 480 |
| atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt | 540 |
| caggcacaca gagaaacaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa | 600 |
| cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct | 660 |
| gagaaaccga aaggagagca gttgaaagca atgatgggtg acaccaccat acttggcctt | 720 |
| gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc | 780 |

aaagatgtaa tgcttcagct cctccgtgaa caatttcctg aagccaatga ctttggaagt 840
 gaggttattc caggtgcaac cagcattgga aagaggggttc aggcttatct gtatgatggt 900
 tactgggaag atatcggtac cattgcgga ttttataatg caaacttggg aataaccaag 960
 aagccaatac cagatttcag cttctatgac cgttttgctc caatttatac acaacctcga 1020
 cacctgccac cttcaaaggt tcttgatgct gatgtgacag acagtgttat tggatgaagga 1080
 tgtgttatta aaaactgcaa gataaacat tctgtagttg gactccgatc ttgcataatct 1140
 gaaggtgcta tcatagagga cagtttacta atgggtgcgg actactatga gacagaagct 1200
 gataaaaaac tccttgccga aaaaggtggc attcctattg gtattgggaa aaattcatgc 1260
 atcaggagag caatcattga caagaatgct cgaattggag acaatgttaa gataactcaat 1320
 gctgacaatg ttcaagaagc tgcaatggag acagacgggt acttcatcaa aggtggaatt 1380
 gtcacagtga tcaaggatgc tttactccct agtgaacag ttata 1425

<210> 2
 <211> 475
 <212> PRT
 <213> zea mays

<400> 2

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
 1 5 10 15
 Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
 20 25 30
 Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
 35 40 45
 Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
 50 55 60
 Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
 65 70 75 80
 Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
 85 90 95
 Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
 100 105 110
 Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
 115 120 125
 Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
 130 135 140

| | | | |
|---|-----|-----|-----|
| Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val | | | |
| 145 | 150 | 155 | 160 |
| Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr | | | |
| | 165 | 170 | 175 |
| Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val | | | |
| | 180 | 185 | 190 |
| Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met | | | |
| | 195 | 200 | 205 |
| Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys | | | |
| | 210 | 215 | 220 |
| Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu | | | |
| 225 | 230 | 235 | 240 |
| Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile | | | |
| | 245 | 250 | 255 |
| Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe | | | |
| | 260 | 265 | 270 |
| Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser | | | |
| | 275 | 280 | 285 |
| Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp | | | |
| | 290 | 295 | 300 |
| Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys | | | |
| 305 | 310 | 315 | 320 |
| Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr | | | |
| | 325 | 330 | 335 |
| Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val | | | |
| | 340 | 345 | 350 |
| Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile | | | |
| | 355 | 360 | 365 |
| Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile | | | |
| | 370 | 375 | 380 |
| Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala | | | |
| 385 | 390 | 395 | 400 |
| Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly | | | |
| | 405 | 410 | 415 |
| Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile | | | |
| | 420 | 425 | 430 |
| Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala | | | |
| | 435 | 440 | 445 |

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
 450 455 460

Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
 465 470 475

<210> 3
 <211> 1425
 <212> DNA
 <213> zea mays

<400> 3
 atggacatgg ctttggcgtc taaagcctcc cctccgccat ggaatgccac cgccgccgag 60
 cagccaattc caaagcgtga caaagccgct gcaaatgatt caacatgyct caatcctcaa 120
 gctcatgata gtgttcttgg aatcattctg ggaggtggtg ctgggactag attgtacccc 180
 ttgacaaaga agcgtgccaa gcctgcagtg ccattgggtg ccaactatag actgattgat 240
 attcctgtca gcaattgtct caacagcaac atatccaaga tctatgtgct aacgcaatth 300
 aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtag 360
 aagaatgaag ggtttgttga agtcttagct gcacagcaga gccagataa tccaaactgg 420
 tttcagggta ctgcagatgc tgtaaggcag tacttgtggt tgtttgagga gcataatgtg 480
 atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt 540
 caggcacaca gagaacaaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa 600
 cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct 660
 gagaaaccga aaggagagca gttgaaagca atgatggttg acaccaccat acttggcctt 720
 gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc 780
 aaagatgtaa tgcttcagct cctccgtgaa caatttcttg aagccaatga ctttggaagt 840
 gaggttattc caggtgcaac cagcattgga aagaggggtc aggcttatct gtatgatggt 900
 tactgggaag atatcggtac cattgcggca ttttataatg caaacttggg aataaccaag 960
 aagccaatac cagatttcag cttctatgac cgttttgctc caatttatac acaacctcga 1020
 cacctgccac cttcaaaggt tcttgatgct gatgtgacag acagtgttat tggatgaagga 1080
 tgtgttatta aaaactgcaa gataaaccat tctgtagttg gactccgac ttgcatactt 1140
 gaaggtgcta tcatagagga cagtttacta atgggtgctg actactatga gacagaagct 1200
 gataaaaaac tccttgccga aaaaggtggc attcctattg gtattgggaa aaattcatgc 1260
 atcaggagag caatcattga caagaatgct cgaattggag acaatgttaa gatactcaat 1320

gctgacaatg ttcaagaagc tgcaatggag acagacgggt acttcatcaa aggtggaatt 1380

gtcacagtga tcaaggatgc ttacttcct agtggacag ttata 1425

<210> 4

<211> 475

<212> PRT

<213> zea mays

<400> 4

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
1 5 10 15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
20 25 30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
35 40 45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
100 105 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
130 135 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145 150 155 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
165 170 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
180 185 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
210 215 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu

| | | | |
|---|-----|-----|-----|
| 225 | 230 | 235 | 240 |
| Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile | | | |
| 245 | 250 | 255 | |
| Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe | | | |
| 260 | 265 | 270 | |
| Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser | | | |
| 275 | 280 | 285 | |
| Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp | | | |
| 290 | 295 | 300 | |
| Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys | | | |
| 305 | 310 | 315 | 320 |
| Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr | | | |
| 325 | 330 | 335 | |
| Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val | | | |
| 340 | 345 | 350 | |
| Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile | | | |
| 355 | 360 | 365 | |
| Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile | | | |
| 370 | 375 | 380 | |
| Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala | | | |
| 385 | 390 | 395 | 400 |
| Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly | | | |
| 405 | 410 | 415 | |
| Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile | | | |
| 420 | 425 | 430 | |
| Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala | | | |
| 435 | 440 | 445 | |
| Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile | | | |
| 450 | 455 | 460 | |
| Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile | | | |
| 465 | 470 | 475 | |

<210> 5

<211> 1428

<212> DNA

<213> zea mays

<400> 5

atggacatgg ctttggcgtc taaagcctcc cctccgccat ggaatgccac cgccgccgag

60

| | | | | | | |
|-------------|------------|------------|-------------|-------------|-------------|------|
| cagccaattc | caaagcgtga | caaagccgct | gcaaatgatt | caacarcata | cctcaatcct | 120 |
| caagctcatg | atagtgttct | tggaatcatt | ctgggagggtg | gtgctgggac | tagattgtac | 180 |
| cccttgacaa | agaagcgtgc | caagcctgca | gtgccattgg | gtgccaaacta | tagactgatt | 240 |
| gatattcctg | tcagcaattg | tctcaacagc | aacatatcca | agatctatgt | gctaacgcaa | 300 |
| tttaactctg | cttcctctaa | ccgtcacctc | tcaagagcct | acgggagcaa | cattggaggg | 360 |
| tacaagaatg | aagggtttgt | tgaagtctta | gctgcacagc | agagcccaga | taatccaaac | 420 |
| tggtttcagg | gtactgcaga | tgctgtaagg | cagtacttgt | ggttgtttga | ggagcataat | 480 |
| gtgatggaat | ttctaattct | tgctggcgat | cacctgtacc | ggatggacta | tgaaaagttc | 540 |
| attcaggcac | acagagaaac | aatgctgat | attaccgttg | ctgccctacc | gatggatgag | 600 |
| aaacgtgcaa | ctgcatttgg | cctcatgaaa | attgatgaag | aaggagggat | cattgagttt | 660 |
| gctgagaaac | cgaaaggaga | gcagttgaaa | gcaatgatgg | ttgacaccac | catacttggc | 720 |
| cttgatgacg | tgagggcaaa | ggaaatgcct | tatattgcta | gcatgggtat | ctatgttttc | 780 |
| agcaaagatg | taatgcttca | gtcctccgt | gaacaatttc | ctgaagccaa | tgactttgga | 840 |
| agtgaggtta | ttccagggtc | aaccagcatt | ggaaagaggg | ttcaggctta | tctgtatgat | 900 |
| ggttactggg | aagatatcgg | taccattgcg | gcattttata | atgcaaactt | gggaataacc | 960 |
| aagaagccaa | taccagattt | cagcttctat | gaccgttttg | ctccaattta | tacacaacct | 1020 |
| cgacacctgc | caccttcaaa | ggttcttgat | gctgatgtga | cagacagtgt | tattggtgaa | 1080 |
| ggatgtgtta | ttaaaaactg | caagataaac | cattctgtag | ttggactccg | atcttgcata | 1140 |
| tctgaagggtg | ctatcataga | ggacagttta | ctaatgggtg | cggactacta | tgagacagaa | 1200 |
| gctgataaaa | aactccttgc | cgaaaaaggt | ggcattccta | ttggtatttg | gaaaaattca | 1260 |
| tgcatcagga | gagcaatcat | tgacaagaat | gctcgaattg | gagacaatgt | taagatactc | 1320 |
| aatgctgaca | atgttcaaga | agctgcaatg | gagacagacg | ggtacttcat | caaagggtgga | 1380 |
| attgtcacag | tgatcaagga | tgctttactc | cctagtggaa | cagttata | | 1428 |

<210> 6

<211> 476

<212> PRT

<213> zea mays

<400> 6

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala

1

5

10

15

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Ala | Glu | Gln | Pro | Ile | Pro | Lys | Arg | Asp | Lys | Ala | Ala | Ala | Asn | 20 | 25 | 30 |
| Asp | Ser | Gln | Thr | Tyr | Leu | Asn | Pro | Gln | Ala | His | Asp | Ser | Val | Leu | Gly | 35 | 40 | 45 |
| Ile | Ile | Leu | Gly | Gly | Gly | Ala | Gly | Thr | Arg | Leu | Tyr | Pro | Leu | Thr | Lys | 50 | 55 | 60 |
| Lys | Arg | Ala | Lys | Pro | Ala | Val | Pro | Leu | Gly | Ala | Asn | Tyr | Arg | Leu | Ile | 65 | 70 | 75 |
| Asp | Ile | Pro | Val | Ser | Asn | Cys | Leu | Asn | Ser | Asn | Ile | Ser | Lys | Ile | Tyr | 85 | 90 | 95 |
| Val | Leu | Thr | Gln | Phe | Asn | Ser | Ala | Ser | Leu | Asn | Arg | His | Leu | Ser | Arg | 100 | 105 | 110 |
| Ala | Tyr | Gly | Ser | Asn | Ile | Gly | Gly | Tyr | Lys | Asn | Glu | Gly | Phe | Val | Glu | 115 | 120 | 125 |
| Val | Leu | Ala | Ala | Gln | Gln | Ser | Pro | Asp | Asn | Pro | Asn | Trp | Phe | Gln | Gly | 130 | 135 | 140 |
| Thr | Ala | Asp | Ala | Val | Arg | Gln | Tyr | Leu | Trp | Leu | Phe | Glu | Glu | His | Asn | 145 | 150 | 155 |
| Val | Met | Glu | Phe | Leu | Ile | Leu | Ala | Gly | Asp | His | Leu | Tyr | Arg | Met | Asp | 165 | 170 | 175 |
| Tyr | Glu | Lys | Phe | Ile | Gln | Ala | His | Arg | Glu | Thr | Asn | Ala | Asp | Ile | Thr | 180 | 185 | 190 |
| Val | Ala | Ala | Leu | Pro | Met | Asp | Glu | Lys | Arg | Ala | Thr | Ala | Phe | Gly | Leu | 195 | 200 | 205 |
| Met | Lys | Ile | Asp | Glu | Glu | Gly | Arg | Ile | Ile | Glu | Phe | Ala | Glu | Lys | Pro | 210 | 215 | 220 |
| Lys | Gly | Glu | Gln | Leu | Lys | Ala | Met | Met | Val | Asp | Thr | Thr | Ile | Leu | Gly | 225 | 230 | 235 |
| Leu | Asp | Asp | Val | Arg | Ala | Lys | Glu | Met | Pro | Tyr | Ile | Ala | Ser | Met | Gly | 245 | 250 | 255 |
| Ile | Tyr | Val | Phe | Ser | Lys | Asp | Val | Met | Leu | Gln | Leu | Leu | Arg | Glu | Gln | 260 | 265 | 270 |
| Phe | Pro | Glu | Ala | Asn | Asp | Phe | Gly | Ser | Glu | Val | Ile | Pro | Gly | Ala | Thr | 275 | 280 | 285 |
| Ser | Ile | Gly | Lys | Arg | Val | Gln | Ala | Tyr | Leu | Tyr | Asp | Gly | Tyr | Trp | Glu | 290 | 295 | 300 |
| Asp | Ile | Gly | Thr | Ile | Ala | Ala | Phe | Tyr | Asn | Ala | Asn | Leu | Gly | Ile | Thr | 305 | 310 | 315 |
| | | | | | | | | | | | | | | | | | | 320 |

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
325 330 335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
340 345 350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
355 360 365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
370 375 380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385 390 395 400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
405 410 415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
420